**P3: 69**

# Identification of genetic transcriptional factors involved in non-*Candida albicans Candida* species biofilm development

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*Candida albicans* is the major cause of candidosis, however recently non-*C. albicans Candida* (NCAC) species have emerged as common pathogens. One of the most important virulence factors is the ability to form biofilms that have important clinical repercussions due to their increased resistant to antifungal therapy. In the case of *C. albicans*, the transcriptional network of biofilm formation is composed by six transcriptions factors (*BCR1*, *EFG1*, *TEC1*, *NDT80*, *ROB1* and *BRG1*). However, in the case of NCAC species little is known about the influence of these genes in biofilm formation. Thus, in order to identify targets to be used as biofilm controllers in NCAC species it was characterized the role of *BCR1*, *EFG1* and *TEC1* genes on *C. parapsilosis* and *C. glabrata* species biofilm formation. After planktonic cells and biofilms grown, the RNAs were extracted and the expression levels of *BCR1*, *EFG1* and *TEC1* compared by quantitative real time PCR. CFUs enumeration and crystal violet staining were used to quantify biofilm formation. The results demonstrated that in both *Candida* species all genes are expressed but in a species and lifestyle dependent manner. Specifically, in opposite to observed in *C. glabrata*, *BCR1* and *TEC1* expression levels, are higher in biofilm than in planktonic cells of C. parapsilosis. Interestingly the *EFG1* levels of expression was superior to 100% in both conditions for *C. parapsilosis*, however higher in planktonic cells. Thus, it is possible to assume that *BCR1*, *TEC1* and *EFG1* are biofilm regulators in *C. parapsilosis*, as in *C. albicans*, but not in *C. glabrata* and they could be suggested to be used as future targets to control *C. parapsilosis* biofilm formation.